

## Correction

## Protocol for detecting rare and common genetic associations in whole-exome sequencing studies using MAGICpipeline

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<https://doi.org/10.1016/j.xpro.2024.102841>

(STAR Protocols 5, 102806; March 15, 2024)

Due to a production error, reference 1 was displayed incorrectly in the originally published version of this protocol. The incorrect version was as follows:

Su, J., Huang, F., Tian, Y., Tian, R., Qianqian, G., Bello, S.T., Zeng, D., Jendrichovsky, P., Lau, C.G., Xiong, W., et al. (2023). Sequencing of 19,219 exomes identifies a low-frequency variant in FKBP5 promoter predisposing to high myopia in a Han Chinese population. *Cell Rep.* 42, 113467.

The correct reference is below:

Su, J., Yuan, J., Xu, L., Xing, S., Sun, M., Yao, Y., Ma, Y., Chen, F., Jiang, L., Li, K., et al. (2023). Sequencing of 19,219 exomes identifies a low-frequency variant in FKBP5 promoter predisposing to high myopia in a Han Chinese population. *Cell Rep.* 42, 112510.

Cell Press apologizes for any confusion this may have caused.

